

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: DAVID GUZO Examiner #: 70677 Date: 7/27/04
 Art Unit: 1636 Phone Number: (571) 272-0767 Serial Number: 10/032585
 Mail Box and Bldg Room Location: RA: 2A79 Results Format Preferred (circle): PAPER DISK E-MAIL
Mailbox: 2C70

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or novelty of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc., if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

*Please run a regular + interference sequence search
 on SEQ ID NO: 4068 and 5068.*

*4068 NA 26
 5068 1 20*

*Thanks**04*

*Gu2585
 7/28 3h*

STAFF USE ONLY

| | Type of Search | Vendors and cost where applicable |
|------------------------------------|-----------------------|-----------------------------------|
| Searcher: _____ | NA Sequence (#) _____ | STN _____ |
| Searcher Phone #: _____ | AA Sequence (#) _____ | Dialog _____ |
| Searcher Location: _____ | Structure (#) _____ | Questel/Orbit _____ |
| Date Searcher Picked Up: _____ | Bibliographic _____ | Dr.Link _____ |
| Date Completed: _____ | Litigation _____ | Lexis/Nexis _____ |
| Searcher Prep & Review Time: _____ | Fulltext _____ | Sequence Systems _____ |
| Clerical Prep Time: _____ | Patent Family _____ | WWW/Internet _____ |
| Online Time: _____ | Other _____ | Other (specify): _____ |

Db 34539 ATTTTCATTAGCTTCAAGCTATGAAACCC-----TTGGATGAGAGAAAGCTTACCG 34592
 QY 596 GAGTGTGTTGGATCTATTTTACAAATCCCTTGCATCCAGTGGCAGTGGTTGGAAA 655
 Db 34593 GTATTACATTAATCTTACTTCACTTCTGTACCCCAAGTTATCTTGGTGTGAGG 34652
 QY 656 CCAATGACTCCAGCAACAT-----TAGACCAACAGACACAGCTTTCTTATGTG 709
 Db 34653 CTCTATGAGCAAGAGCTTTCTTCTTCATGGCCCTGAGAGCACTTAAGCTATATGA 34712
 QY 710 CTCTATATATGAGAGGAGCTGATGCGCTGCTGCTAATCCAGCT---CAAGTGCTT 766
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 Db 34773 TCACTGCAACATTTTGGCCGTAAGCTAGTCCCAAGTTGAGGAGGTGATGATGCACT 34832
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 Db 35004 CTCTGCGCTTACAGCTGATTAATGATC 35030

RESULT 9
 LOCUS NC00038 1453 bp mRNA linear PLN 29-JUL-1992
 DEFINITION N. crassa mRNA MOM38.
 ACCESSION X56883
 VERSION X56883.1 GI:3025
 KEYWORDS outer membrane protein.
 SOURCE Neurospora crassa
 ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 REFERENCE 1 (bases 1 to 1453)
 Kiebler, M., Pfaffler, R., Solinger, T., Griffiths, G., Horstmann, H., Pfanner, N., and Neupert, W.
 Identification of a mitochondrial receptor complex required for recognition and membrane insertion of precursor proteins
 JOURNAL Nature 348 (6302), 610-616 (1990)
 MEDLINE 91066945
 PUBMED 2174514
 TITLE 2 (bases 1 to 1453)
 AUTHORS Kiebler, M.
 DIRECT SUBMISSION
 JOURNAL Submitted (26-JUN-1992) M. Kiebler, Institut f. Physiologische Chemie, der LMU Muenchen, Goethe 33, 8 Muenchen 2, FRG
 FEATURES
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 1.1453
 /location/Qualifiers
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 /organism="Neurospora crassa"
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ORIGIN
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 Best Local Similarity 51.8%; Pred. No. 4,4e-20;
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138 CGATGTTTATATCTATTAACGACACCGTAATCTTTGGATTAACCAACCGGGAAC 197
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 Db 157 GATGAGACATCGCCCGGACAGGTCCACCGCATACCTCTCACCACCTACATGTTCTC 216
 QY 258 AGGTTGAGAGCTGATTTAAACAAAGCTTTTCATGATGATCCAGCATTCGAAACATCCA 317
 Db 217 TGGCTCGCGGCGGACCTGACCAAGGCTTTCAAGCTGCGCCCTCTTCCAAAGTTTCCA 276
 QY 318 CACTTAAGTATGATGATCCAAAGTTTACAGCGCTATGCTTACAGGCTTATATGCGAC 377
 Db 277 CCAAGTTTCCATGGG---CGAGAGGTTGAACCTTATGCTTGTGCTGCTCTTACGGAAC 333
 QY 378 CGATGATTTATTTCTTACAGATTAACATGACATGATTAATCATTTCTGATGAATCAA 437
 Db 334 CAACCAATCTTGGCTAGGTTAAGCTGACCAAGAGGCGCTCTCTCCAAAGATTCAA 393
 QY 438 TTAGGATGGGACAAATCAACATTTTCCAAAGTCAATTTCAATTTAGCTATGACCAAC 497
 Db 394 CTACAGATGGGGTGAACGACGACATCAACCAAGACGAGTTTCGATGTTGGCGGCA--- 450
 QY 498 ATCCATGATCCAAATTGACAAACATTAATCAAGTAAATGATTTCTATCAATGCAAAAC 557
 Db 451 GGAATGCGCCAGTTGAGATGACATCAACCTTGGCGAGCATTTAGTGCCCTCCCAAGGC 510
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 QY 618 ACATCTCTTATCCATCCAGTTGGCAGTGGCTTTGAAACCATGATCCCAAGCAACCAT 677
 Db 628 CACTCAAGGCGCCGACACCGCTATCTCTCTTCCCGGTACAAAGCGGATGAGGT 687
 QY 735 CGGCTGCTCAACTCCCAAGCTCAAGTGTGATTTGCAAGTTTCTGAGGAAGATGAC 794
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 Db 748 GGAATAGGTCAGAGCTGTGTTGA-----TATGACGTACTCTGTGC 789
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 QY 915 GTATGAATACAGAACTGCGCTTTTCAAGAGTCAATGATTAAGAGGTAAAGTCAAGTGC 974
 Db 850 GTAGAGCTTCAAGATGCACTTCAAGGCTCAGATGACTCCAAAGGCAAGCTCAAGCTG 909
 QY 975 ATTTTGAAGAAAGAG 989

DB 910 CTGGCTGAGAGCG 924

RESULT 10

CNS101D1 660 bp mRNA linear PLN 03-SEP-1999

LOCUS Botrytis cinerea strain T4 cDNA library under conditions of nitrogen deprivation.

DEFINITION

ACCESSION AL117029

VERSION AL117029.1 GI:58322245

KEYWORDS cDNA library; nitrogen deprivation.

SOURCE Botryotinia fuckeliana

ORGANISM Botryotinia fuckeliana

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Leotiomycetes; Helotiales; Sclerotiniaceae; Botryotinia.

REFERENCE 1 (bases 1 to 660)

Bitton, F., Lewis, C., Fortini, D., Pradier, J.M. and Brygoo, Y. Submitted (01-SEP-1999) Phytopathologie, INRA, route de St Cyr, 78020 Versailles, France

2 (bases 1 to 660)

Genoscope.

Direct Submission

Submitted (01-SEP-1999) Genoscope - Centre National de Sequencage : CP 5706 91057 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

COMMENT The cDNA library to be analyzed within the framework of this project was created using a Botrytis cinerea strain which was grown under conditions of nitrogen deprivation, which is the normal situation for B. cinerea during its development on its host plant. The library was produced in an oriented direction, in the pBSII vector.

FEATURES

source

Location/Qualifiers

1..660

/organism="Botryotinia fuckeliana"

/mol_type="mRNA"

/strain="T4"

/db_xref="taxon:40559"

/note="Genoscope sequence ID : W40B111"

ORIGIN

Query Match 10.6%; Score 124.8; DB 8; Length 660;

Best Local Similarity 56.0%; Pvec. No. 5.7e-18;

Matches 344; Conservative 0; Mismatches 252; Indels 18; Gaps 5;

439 TACGATGGGACCAATCAACATTCACAGTCACTTACATTAAGCTCAGACACCA 498

11 TACAGATGAGCTCAGCTTCTGTTACAGACGAGACTTCAAGTCCGCCCGTCA---A 67

499 TCCAGATGCCATTTGAAACAAGATTAAAGCTAATGATTTCTTATCAATGTCAAACT 558

68 GCTATGATGCAATTAAGACACGAGTAAACGACAAAGTTTCAAGCTTCAATCAATCT 127

559 TTGAACCTTAATTTTATCAAGTAAATCAATCAAGTGAAGTTGTTGGATCTATTTTA 618

128 CTCACACCT---TCGATACCTGACGAGAGATTAACGGTATTTTCATTTGCAATTTTA 184

619 CAATCTTGTATCAATCAAGTGGCACTCGTTTGAACCAATGTAAGTCAACCAACCTT- 677

185 CAAGCTGATCTCAAAACCTTCTTGGATTTGAGGTGCTGTCGCAACGGCGGCAATG 244

678 --AGCACACACAGACAGCTGTTTCTATATGCTCTTATTAAGACGCAACTGGATC 735

245 AACCAAGAGCCGGAATCGCGGTATCATATGTCGCAAAATACAGAGGTAGATGGATT 304

736 GCGTCTGCTCACTCCAGCTCAAGTCTTGAATGTAATTTCTGAGAAAGTCACT 795

305 GCTAGTCTCAATTCAGAGCGGAGAGAGCTGTCAACATCGTTCTGAGAAAGTTGACA 364

796 GATTAAGTGAAGCTGTTTGAACCAACCAAGTCTGCACTAAGAAACAAGTTGCTGAT 855

365 GATAAGTCAAGAGCTGCTGATCTTAATTCGAATTCGAGAGGTGTCTGAGGCTGG- 423

DB 910 CTGGCTGAGAGCG 924

RESULT 11

NCBI0104/C 90763 bp DNA linear PLN 18-JAN-2002

LOCUS Neurospora crassa DNA linkage group V BAC contig B10H4.

DEFINITION

ACCESSION AL670010

VERSION AL670010.1 GI:18376274

KEYWORDS Neurospora crassa

SOURCE Neurospora crassa

ORGANISM Neurospora crassa

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Eurotiomycetidae; Sordariiales; Sordariaceae; Neurospora.

REFERENCE 1

Schulte, U., Aign, V., Hohelsel, J., Brandt, P., Fartmann, B., Holland, R., Nyakatura, G., Wewes, H.M. and Mannhaupt, G. Unpublished

2 (bases 1 to 90763)

German Neurospora genome project.

Direct Submission

Submitted (18-JAN-2002) MIPS, Institut fuer Bioinformatik, GSF-Forschungszentrum fuer Umwelt und Gesundheit, GmbH, Ingolstaedter Landstrasse 1, D-85764 Neuberg, FRG, E-mail: G.Mannhaupt@gsf.de Project Coordinator: Ulrich Schulte, Institute of Biochemistry, Heinrich-Heine-University, D-40225 Dueseldorf, E-mail: ulrich.schulte@uni-duesseldorf.de

COMMENT This contig is an assembly of BAC 10H4 from 1 to: 70452, strain OR74a, and cosmid 6B10 from 70453 to: 90763, cosmid library pIOR1876xh, strain 74-OR-23-1A; BAC and cosmid clones are available at the Fungal Genetic Stock Center, <http://www.fgsc.net>. Sequencing was performed by MWD Biotech AG, Ebersberg, Germany, <http://www.mwgdna.com>. Information on performance of analysis and a more detailed annotation of this entry and other sequences of linkage groups II and V can be viewed at: <http://mbe.gsf.de/proj/neurospora>.

FEATURES

source

Location/Qualifiers

1..90763

/organism="Neurospora crassa"

/mol_type="genomic DNA"

/db_xref="taxon:5141"

/chromosome="2"

1..34518

/note="overlap to BAC contig 18F11, please refer to this entry for analysis and annotation"

31067..35516

/gene="B10H4.010"

/join(31067..31724,31779..31895,31970..32537,32610..32947,33009..33198,33290..35516)

/gene="B10H4.010"

/note="similarity to cholesterol oxidase (EC 1.1.3.6) precursor, Streptomyces sp., PIR:A12260"

/codon_start=1

/product="related to cholesterol oxidase precursor"

/protein_id="CAD21388.1"

/db_xref="GI:18376275"

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/translation="MDRLAHQNSNAPSPPTPACSGRLGVKXTDTAGLFGVSTHTNG

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| Db | 123 | GTTTTCATTTATCATCAAGATGTTTATATCATATTAACGAAACCCGTAATCATTTGGGA | 252 |
| OY | 151 | TTAACCAACCCGGGAACATTTGAAAACTTGAACAGAGAGTTGCCGTGATGTGTTTTG | 240 |
| Db | 253 | TTAACCAACCCGGGAACATTTGAAAACTTGAACAGAGAGTTGCCGTGATGTGTTTTG | 312 |
| OY | 241 | GGTCAATATTTCTTCAACAGGGTTGAGAGGTGATTTAAACAAAGCCTTTCCATGATGCA | 300 |
| Db | 313 | GGTCAATATTTCTTCAACAGGGTTGAGAGGTGATTTAAACAAAGCCTTTCCATGATGCA | 372 |
| OY | 301 | GCATTCCAAACATTCACACTTTAAGTATTTGATCCCAAGTTTATCCAGCCATATGCTTC | 360 |
| Db | 373 | GCATTCCAAACATTCACACTTTAAGTATTTGATCCCAAGTTTATCCAGCCATATGCTTC | 432 |
| OY | 351 | AGTGGCTTATATGCCCACCGATGATTTATTTCTTCAACAGTTAATTTGACATGATTTATCA | 420 |
| Db | 433 | AGTGGCTTATATGCCCACCGATGATTTATTTCTTCAACAGTTAATTTGACATGATTTATCA | 492 |
| OY | 421 | TTTTCTGTGATGATCAATATACGGATGGGACAATCAATCAATTTCCAAAGTCACTTACA | 480 |
| Db | 493 | TTTTCTGTGATGATCAATATACGGATGGGACAATCAATCAATTTCCAAAGTCACTTACA | 552 |
| OY | 481 | TTAGCTCATGACAAACCATCATGATTCATTTAGAACAAAGATTTCAAGCTAATGATGT | 540 |
| Db | 553 | TTAGCTCATGACAAACCATCATGATTCATTTAGAACAAAGATTTCAAGCTAATGATGT | 612 |
| OY | 541 | TCTATCAATGTCAAAAAGTTGATACCTTAATCTTTATACAGTAATGAATTCAGTGAAGT | 600 |
| Db | 613 | TCTATCAATGTCAAAAAGTTGATACCTTAATCTTTATACAGTAATGAATTCAGTGAAGT | 672 |
| OY | 601 | GTTGTGGATCTATTTTAAACATCTCTGTTCATCCAAAGTTGGCAGTGGTTGAAACCATG | 660 |
| Db | 673 | GTTGTGGATCTATTTTAAACATCTCTGTTCATCCAAAGTTGGCAGTGGTTGAAACCATG | 732 |
| OY | 661 | TATCTCCAGCAACCATTTAGCAACCAACAGACAGCTGTTCTTATGTTGCTCGTATATAT | 720 |
| Db | 733 | TATCTCCAGCAACCATTTAGCAACCAACAGACAGCTGTTCTTATGTTGCTCGTATATAT | 792 |
| OY | 721 | GCAGGCACTGGATGCGCTGCTCAACCTCCAAAGCTCAAGGCTTTGATTTGCAAGTTTC | 780 |
| Db | 793 | GCAGGCACTGGATGCGCTGCTCAACCTCCAAAGCTTTGATTTGCAAGTTTC | 852 |
| OY | 781 | TGAGAAAGGTCACTGATTAAGTCGAAGCTGTTTGAAGAACCAAGTTGCTGCACATAG | 840 |
| Db | 853 | TGAGAAAGGTCACTGATTAAGTCGAAGCTGTTTGAAGAACCAAGTTGCTGCACATAG | 912 |
| OY | 841 | AAACAAGTGTGCTGATCCATTTATGSGTGTGTTTGAACCAAGTATTTGAAGGTCAACT | 900 |
| Db | 913 | AAACAAGTGTGCTGATCCATTTATGSGTGTGTTTGAACCAAGTATTTGAAGGTCAACT | 972 |
| OY | 901 | ACTATGTGTGCCAAGTATGAATACAGAACTGCCCTTTCAAGAGTCAATTTGATCAAG | 960 |
| Db | 973 | ACTATGTGTGCCAAGTATGAATACAGAACTGCCCTTTCAAGAGTCAATTTGATCAAG | 1032 |
| OY | 961 | GCTAAGATCACTGCACTTTTGAAGAAAGGAATCAGCACTGTTTCCATATATATTTCT | 1020 |
| Db | 1033 | GCTAAGATCACTGCACTTTTGAAGAAAGGAATCAGCACTGTTTCCATATATATTTCT | 1092 |
| OY | 1021 | GGAGAAATTTGATCAATTTCAAGAAATACATCTCGTTGGGTTGGGTTGCAATTTGAGGCT | 1080 |
| Db | 1093 | GGAGAAATTTGATCAATTTCAAGAAATACATCTCGTTGGGTTGGGTTGCAATTTGAGGCT | 1156 |
| OY | 1081 | GCTGTAATGAACAAATTGATTTAATGCAACAAGTTTATGTAACGCTAATGTAATCTT | 1140 |
| Db | 1153 | GCTGTAATGAACAAATTGATTTAATGCAACAAGTTTATGTAACGCTAATGTAATCTT | 1212 |
| OY | 1141 | ATCCAGGTGCGCCAGCTCCAGGTCCTTGT | 1171 |
| Db | 1213 | ATCCAGGTGCGCCAGCTCCAGGTCCTTGT | 1243 |

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RESULT 8
US-10-603-113-3520
; Sequence 3520, Application US/10603113
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/10/603, 113
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US/09/248,796
; PRIOR FILING DATE: 1999-02-12
; NUMBER OF SEQ ID NOS: 28206
; SEQ ID NO 3520
; LENGTH: 1260
; TYPE: DNA
; ORGANISM: Candida albicans
US-10-603-113-3520

Query Match      99.3%; Score 1164.6; DB 53; Length 1260;
Best Local Similarity 99.7%; Pred. No. 1.3e-306;
Matches 1167; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1  ATGTCGAACAGATTAATCCACCATTTAGGCTCTACTGACATAGCCAAAGTTGAGCATCCCA 60
DB      73  ATGTCGAACAGATTAATCCACCATTTAGGCTCTACTGACATAGCCAAAGTTGAGCATCCCA 132

QY      61  ACGTTGGCTCAAGGACACACCGGACCGAACCGAAAGAAATGATGTGTCATAACCCA 120
DB      133  ACGTTGGCTCAAGGACACCGGACCGAACCGAAAGAAATGATGTGTCATAACCCA 192

QY      121  GTTTTCAGTTACATCAACGATGTTATATCATCTATTAACGACACCGTAATCATTTGGGA 180
DB      193  GTTTTCAGTTACATCAACGATGTTATATCATCTATTAACGACACCGTAATCATTTGGGA 252

QY      181  TTAAACCAACCCGGGAACAATTGAAACTTGAACAGAGAGTTGCCGTGATGTTTGG 240
DB      253  TTAAACCAACCCGGGAACAATTGAAACTTGAACAGAGAGTTGCCGTGATGTTTGG 312

QY      241  GGTCAATATTTCTTCACAGGGTTGAGAGCTGATTTAAACAAAGCCTTTCCATGATGCCA 300
DB      313  GGTCAATATTTCTTCACAGGGTTGAGAGCTGATTTAAACAAAGCCTTTCCATGATGCCA 372

QY      301  GCATTCGAACATCCGACACCTTAAAGTATGGAATCCAGCGTTTACCAAGCCTATGCTTTC 360
DB      373  GCATTCGAACATCCGACACCTTAAAGTATGGAATCCAGCGTTTACCAAGCCTATGCTTTC 432

QY      361  AGTGCCTTATATGCGACCGATGATTAATTTCTTTCACAGATTAACATTGACAAATGATTATCA 420
DB      433  AGTGCCTTATATGCGACCGATGATTAATTTCTTTCACAGATTAACATTGACAAATGATTATCA 492

QY      421  TTTTCGTGTGAATCAATTTACGATGGGACAAATCAACAATTCCAAAGTACATTACAA 480
DB      493  TTTTCGTGTGAATCAATTTACGATGGGACAAATCAACAATTCCAAAGTACATTACAA 552

QY      481  TTAGCTATGAGACAACCATCATGATCAATTTAGAACAGATTACAGCTATATGATGTG 540
DB      553  TTAGCTATGAGACAACCATCATGATCAATTTAGAACAGATTACAGCTATATGATGTG 612

QY      541  TCTATCAATGTCAAAAATTGGAACCCTAATCTTTTATCAGGTAATGAATTCAGTGAAGTT 600
DB      613  TCTATCAATGTCAAAAATTGGAACCCTAATCTTTTATCAGGTAATGAATTCAGTGAAGTT 672

QY      601  GTTGTGGATCTATTTTACAAATCCTGTGCATCCAAAGTTGGAGCTGGTTTGAACAATG 660
DB      673  GTTGTGGATCTATTTTACAAATCCTGTGCATCCAAAGTTGGAGCTGGTTTGAACAATG 732

QY      661  TATCCCAAGAACCATTTAGACACCAACGACGACAGAGCTGTTCTATGTGTGCTCGTTAAT 720
DB      733  TATCCCAAGAACCATTTAGACACCAACGACGACGCTGTTCTATGTGTGCTCGTTAAT 792

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| | | | |
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| QY | 301 | GCATTCGCAACATCCCACTTTAAGATTGATCCAACTTTACAGCCGTAATGCTTC | 360 |
| Db | 373 | GCATTCGCAACATCCCACTTTAAGATTGATCCAACTTTTACAGCCGTAATGCTTC | 432 |
| QY | 361 | AGTGCCTTATATGCAACCGATGATTATTTCTTCAAGTAACTGCAATGATTATCA | 420 |
| Db | 433 | AGTGCCTTATATGCAACCGATGATTATTTCTTCAAGTAACTGCAATGATTATCA | 492 |
| QY | 421 | TTTTTCGGTGAATCAATTACGATGGGACAAATCCAACTTTCCAAAGTCACTTCAA | 480 |
| Db | 493 | TTTTTCGGTGAATCAATTACGATGGGACAAATCCAACTTTCCAAAGTCACTTCAA | 552 |
| QY | 481 | TTTGGCTATGAGACACCATCATGATGATCAATTGAAACAATATTCAAGCTAATGATTGT | 540 |
| Db | 553 | TTTGGCTATGAGACACCATCATGATGATCAATTGAAACAATATTCAAGCTAATGATTGT | 612 |
| QY | 541 | TCTATCATATGCAAACTTTGAACCCCTTACTTTTATCAGGTAAATGAAATTCAGTGGAGTT | 600 |
| Db | 613 | TCTATCATATGCAAACTTTGAACCCCTTACTTTTATCAGGTAAATGAAATTCAGTGGAGTT | 672 |
| QY | 601 | GTTGTTGGAATCTATTAAATCTTGTCAATCCAAAGTTGGCAGTCGTTTGGAAACATG | 660 |
| Db | 673 | GTTGTTGGAATCTATTAAATCTTGTCAATCCAAAGTTGGCAGTCGTTTGGAAACATG | 732 |
| QY | 661 | TATCCCAAGACCAATAGACACCAACGACAGACGCTGTTCTATGTTGTCGCTATAT | 720 |
| Db | 733 | TATCCCAAGACCAATAGACACCAACGACAGACGCTGTTCTATGTTGTCGCTATAT | 792 |
| QY | 721 | GCAGGCAACTGATGCGCTGTGCTCAATCCAACTCAAGTGCCTTGATTGCAAGTTTC | 780 |
| Db | 793 | GCAGGCAACTGATGCGCTGTGCTCAATCCAACTCAAGTGCCTTGATTGCAAGTTTC | 852 |

| | | | |
|----|------|--|------|
| Qy | 781 | TGGGAAGAGCATCGTAAAGGTGAAGACGCGGTTAGAAACCAAGTGGCTGCCAATAG | 844 |
| Db | 853 | TGGAGAAAGGCACTGATAAAGGTGAAGACGCGGTTAGAAACCAAGTGGCTGCCAATAG | 912 |
| Qy | 841 | AAACAAGTGGTCATTCATTAAAGGTTGGTTTGAACCAAGTCATTGAAGGTCAAACT | 900 |
| Db | 913 | AAACAAGTGGTCATTCATTAAAGGTTGGTTTGAACCAAGTCATTGAAGGTCAAACT | 972 |
| Qy | 901 | ACTATTGGTGCAGATGAATGAAATACAGAACTGGCGTTTCAGAGGTCAATTGGATTCAAG | 960 |
| Db | 973 | ACTATTGGTGCAGATGAATGAATACAGAACTGGCGTTTCAGAGGTCAATTGGATTCAAG | 1032 |
| Qy | 961 | GGTAGATCACTGCATTTTGGAAAAGAGAACTAGGCCAATGTTTCCATATATATTTCT | 1022 |
| Db | 1033 | GGTAGATCACTGCATTTTGGAAAAGAGAACTAGGCCAATGTTTCCATATATATTTCT | 1092 |

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Db      1093  GGAAGAAATTGATCAATTCAGAAATACATCTCTGTTGGCTCGGGGTTTGCAATTGAGGCT 115
Qy      1081  GCTGTAATATGACATTCATGATTTATGTAACAAGAGTTTATCTCGAAGCGTTAAATGGTAATCCT 114
Db      1153  GCTGGTAATGACCAATTCATCATCTTTATGTGAACAAGGTTTAGTGAAGCTAAATGGTTATCCT 121
Qy      1141  ATCCAGGTGCTCCAGCTCCAGGTGCTTGT 1171
Db      1213  ATCCCATGTGCTCCAGCTCCAGGTGCTTGT 1243

RESULT 10
US-10-32c-956-3118
; Sequence 3118, Application US/10326556
; GENERAL INFORMATION:
; APPLICANT: Bauer et al.
; TITLE OF INVENTION: Protein Complexes and Methods for their use
; FILE REFERENCE: 220615
; CURRENT APPLICATION NUMBER: US/10/326,956
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